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MPsrch\_PP Protein - Protein database search, using Smith-Waterman algorithm

Run on: Fri Jan 21 14:30:17 2000; MasPar time 6.36 Seconds

330.840 Million cell updates/sec  
Tabular output not generated.

Title: >US-09-176-546-2

Description: (1-99) from US09176546.pep

Perfect Score: 682

Sequence: 1 MADGSSDAAREPRPAPIR.....COPLETLAGLGFALQDLCRQ 99

Scoring table: PAM 150

Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseg35  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33  
34:part34 35:part35 36:part36 37:part37 38:part38  
39:part39

Statistics: Mean 28.682; Variance 122.478; scale 0.234

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	682	100.0	216	37	W72758	Modified human cardiac troponin I
2	682	100.0	216	29	W41573	Modified human cardiac troponin I
3	682	100.0	222	29	W41570	Modified human cardiac troponin I
4	680	99.7	226	26	W18054	Recombinant human myo cardiac troponin I
5	678	99.4	319	29	W41572	Human cardiac troponin I
6	678	99.4	372	29	W41571	Cardiac troponin I/CA
7	669	98.1	153	26	W18053	Recombinant myofibrillar troponin I
8	536	78.6	80	21	W02286	Human troponin I
9	239	35.0	38	12	R66181	Cardiac troponin I
10	233	34.2	35	21	W02285	Human troponin I
11	207	30.4	31	32	W37924	N-terminal amino acid sequence of human cardiac troponin I
12	202	29.6	30	11	R55781	Human cardiac troponin I
13	202	29.6	31	21	W05041	N-terminus of cardiac troponin I
14	202	29.6	31	14	R7352	N-terminal sequence of human cardiac troponin I
15	201	29.5	182	26	W22598	Human fast twitch skeletomuscle troponin I
16	173	25.4	26	11	R55786	Human cardiac troponin I

#### ALIGNMENTS

##### RESULT 1

ID	W72758	standard: Protein; 216 AA.
AC	W72758	(first entry)
DT	13-JUN-1999	
DE	Modified human cardiac troponin I.	
KW	Human cardiac troponin I; troponin I; modified: antigen; stable troponin subunit; cardiac disorder; myocardial damage; heart attack.	
KW		
OS	Homo sapiens.	
OS	Synthetic.	
PN	US5834210-A.	
PD	10-NOV-1998	
PP	31-OCT-1997; 961858	
PR	31-OCT-1997; US-961858--	
PR	23-MAY-1997; US-862613--	
PR	(SPEC) SPECTRAL DIAGNOSTICS INC.	
PI	Liu, S., Shi, Q.	
DR	WPI: 99-00870/01.	
DR	N-PSDB; V67262.	
PT	Recombinant modified human cardiac troponin I and complexes with troponin T and C - for use in assays to determine levels of these proteins, control values in determining extent of cardiac damage	
PT	e.g. in heart attacks	
PT		
PS	Claim 1: Fig 1: 16pp; English.	
CC	The present sequence represents modified human cardiac troponin I.	
CC	Expression in Escherichia coli of the modified troponin I is increased compared to that of the native sequence. The modified troponin I protein sequence with an N-terminal methionine. The present invention describes troponin protein complexes which are useful for the determination of myocardial damage. Troponin I and troponin T have been found to be highly specific markers for cardiac disorders, especially heart attacks. They must be complexed with troponin C to form a stable structure, which is difficult to isolate. Recombinant protein of the trimeric structure allows sufficient quantities to be obtained, so that assays can be performed to accurately determine quantification of troponin complex levels for e.g. control values. The complex can also be used as an antigen to raise antibodies.	
CC	Sequence 216 AA;	



FT	Modified_site	87	/note- "carboxymethylated to prevent dimerisation by inter or intra disulphide bridges"	OS	Chimeric - <i>Cyprinus carpio</i> .
FT	Modified_site	104	/note- "carboxymethylated to prevent dimerisation by inter or intra disulphide bridges"	FH	Key 1..210
FT	Peptide	9..217	/note- "human Troponin I"	FT	Protein /label- HctnI
FT	Peptide	9..161	/note- "CN-Br cleavage fragment"	FT	Protein
FT	Peptide	8..219	/note- "CN-Br cleavage fragment"	FT	FT W09739132-A1.
FT	Peptide	2..4	/note- "CN-Br cleavage fragment"	FT	PN 23-OCT-1997; PR 14-APR-1997; US-833743.
FT	Peptide	5..8	/note- "CN-Br cleavage fragment"	FT	PR 11-APR-1997; US-833743.
FT	Peptide	163..208	/note- "CN-Br cleavage fragment"	FT	PR 16-APR-1996; US-015772.
FT	Peptide	209..19	/note- "CN-Br cleavage fragment"	PA	(UWMI-) UNIV MIAMI.
FT	Peptide	220..226	/note- "CN-Br cleavage fragment"	PI	Potter JD;
FT	Peptide	14..101	/note- "CN-Br cleavage fragment"	DR	WPI; 98-062676/06.
FT	Peptide	PN W09719955-A1.	/note- "CN-Br cleavage fragment"	DR	N-PSDB; V04228.
PD	05-JUN-1997.	PPF 26-NOV-1995; US-164526.	PT Immunassay of mammalian troponin using stable standard for comparison - specifically acid-diethylated solution or its lyophilisate used for diagnosis of cardiac or skeletal muscle damage	PT	Immunoassay of mammalian troponin using stable standard for comparison - specifically acid-diethylated solution or its lyophilisate used for diagnosis of cardiac or skeletal muscle damage
PR	29-NOV-1995; US-164526.	PPF 05-JUN-1997; V04228.	Example 4; Page 71-72; 94pp; English.	PT	Example 4; Page 71-72; 94pp; English.
PA	(DADE) DADE INT INC.	PPF 05-JUN-1997; V04228.	This polypeptide comprises fusion protein with the N-terminal region being human cardiac troponin I (HctnI) and the C-terminal region being carp parvalbumin. It was expressed in <i>E. coli</i> host cells utilising a vector incorporating a poly nucleotide (see V04228) encoding the fusion. The addition of parvalbumin, a calcium binding protein, to HctnI provides more favourable solubility properties to HctnI and to the fusion protein. The invention provides an assay for measuring mammalian, preferably human, troponin in patient sample. The assay includes the step of comparing the level in the sample with a novel troponin protein standard. This may be a storage stable, soluble mammalian troponin, a functional fragment of the troponin, a modified troponin or its functional fragment, a troponin fusion protein or a heteromultimeric troponin complex (see also W41570-75). The method is used to monitor changes in the level of human troponin, particularly for diagnosis of diseases involving damage to heart or skeletal muscle, e.g. acute myocardial infarction. It may also be used to study normal and pathological functions of troponin-expressing tissues.	PT	This polypeptide comprises fusion protein with the N-terminal region being human cardiac troponin I (HctnI) and the C-terminal region being carp parvalbumin. It was expressed in <i>E. coli</i> host cells utilising a vector incorporating a poly nucleotide (see V04228) encoding the fusion. The addition of parvalbumin, a calcium binding protein, to HctnI provides more favourable solubility properties to HctnI and to the fusion protein. The invention provides an assay for measuring mammalian, preferably human, troponin in patient sample. The assay includes the step of comparing the level in the sample with a novel troponin protein standard. This may be a storage stable, soluble mammalian troponin, a functional fragment of the troponin, a modified troponin or its functional fragment, a troponin fusion protein or a heteromultimeric troponin complex (see also W41570-75). The method is used to monitor changes in the level of human troponin, particularly for diagnosis of diseases involving damage to heart or skeletal muscle, e.g. acute myocardial infarction. It may also be used to study normal and pathological functions of troponin-expressing tissues.
Demarco C.	Moriana NA;	PPF 05-JUN-1997; V04228.	Sequence 31 AA;	CC	Sequence 31 AA;
WPI: 97-310526/28.	DR	PPF 05-JUN-1997; V04228.	Query Match 99.4%; Score 678; DB 29; Length 319; Best Local Similarity 99.0%; Pred. No. 1..75-54.	CC	Query Match 99.4%; Score 678; DB 29; Length 319; Best Local Similarity 99.0%; Pred. No. 1..75-54.
PT	Human cardiac Troponin I cyanogen bromide cleaved fragment - used in calibrator or control for troponin I immunoassay	PPF 05-JUN-1997; V04228.	Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	CC	Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
PR	Disclosure: Page 20; 52pp; English.	PPF 05-JUN-1997; V04228.	Db 1 mvdgssdaareprpapirrrsnyrayatephakkskisrasrklqlqlqtake 60	CC	Db 1 mvdgssdaareprpapirrrsnyrayatephakkskisrasrklqlqlqtake 60
PS	The present sequence represents a recombinant form of the cardiac isotype of the myofibrillar contractile protein Troponin I (crtnI).	PPF 05-JUN-1997; V04228.	Qy 1 MADGSSDAAREPRPAPIRRSSNYRAYATEPHAKKSKISASRKLQLKTLIQAKE 60	CC	Qy 1 MADGSSDAAREPRPAPIRRSSNYRAYATEPHAKKSKISASRKLQLKTLIQAKE 60
CC	Troponin I is the inhibitory subunit of Troponin, a thin filament regulatory protein complex which controls calcium sensitivity to the cardiac and striated muscle. CtnI was cleaved with cyanogen bromide, which cleaves at Met residues with a high specificity under acidic conditions, to generate several fragments. A 153 amino acid CNBR-ctnI isoform is used in a calibrator or a control for a TnI immunoassay. The CNBR-ctnI isoform is comparable in molecular weight to a major degradation product of native ctnI in the serum of patients who have experienced myocardial infarction. The peptide has immunological activity to antibodies against TnI. The CNBR-ctnI isoform has an average of 3-4 times more reactivity than rtnI and lower non-specific binding, as measured by radial partition immunoassay. It also has increased stability over the synthetic peptide currently used in the Dade TnI immunoassay.	PPF 05-JUN-1997; V04228.	Db 61 lereaeerrgekgralstrcplelaglgfaelgdcirg 99	CC	Db 61 lereaeerrgekgralstrcplelaglgfaelgdcirg 99
CC	Sequence 226 AA;	PPF 05-JUN-1997; V04228.	Qy 61 LEREAEERRGEKGRALSTRCPELEAGLGFAELQDLCRQ 99	CC	Qy 61 LEREAEERRGEKGRALSTRCPELEAGLGFAELQDLCRQ 99
CC	Query Match 99.7%; Score 680; DB 26; Length 226; Best Local Similarity 99.0%; Pred. No. 1..12e-54; Indels 0; Gaps 0;	FT	RESULT 6	FT	RESULT 5
CC	Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FT	ID W41571 standard; Protein; 372 AA.	FT	ID W41572 standard; Protein; 319 AA.
Db	8 madgssdaareprpapirrrsnyrayatephakkskisrasrklqlqlqtake 67	AC W41571; W41571; W41571; W41571; W41571; W41571; W41571; W41571;	AC W41571; W41571; W41571; W41571; W41571; W41571; W41571; W41571;	AC W41571; W41571; W41571; W41571; W41571; W41571; W41571; W41571;	AC W41571; W41571; W41571; W41571; W41571; W41571; W41571; W41571;
Qy	1 MADGSSDAAREPRPAPIRRSSNYRAYATEPHAKKSKISASRKLQLKTLIQAKE 60	DT 22-JUN-1998 (first entry)	DT 22-JUN-1998 (first entry)	DT 22-JUN-1998 (first entry)	DT 22-JUN-1998 (first entry)
Db	68 lereaeerrgekgralstrcplelaglgfaelgdcirg 106	DE Human cardiac troponin I/carp parvalbumin fusion protein.	DE Cardiac troponin I/cardiac troponin C fusion protein.	DE Cardiac troponin I; troponin C; immunoassay; assay; analysis; human;	DE Cardiac troponin I; troponin C; immunoassay; assay; analysis; human;
Qy	61 LEREAEERRGEKGRALSTRCPELEAGLGFAELQDLCRQ 99	KW cardiac muscle; skeletal muscle; injury; myocardial infarction;	KW cardiac muscle; skeletal muscle; injury; myocardial infarction;	KW cardiac muscle; skeletal muscle; injury; myocardial infarction;	KW cardiac muscle; skeletal muscle; injury; myocardial infarction;
OS	Chimeric - Homo sapiens.	OS	OS	OS	OS

DR WPI: 98-062676/06.  
 DR N-PSDB: V04225.  
 PT Immunoassay of mammalian troponin using stable standard for  
 PT comparison - specifically acid-dialysed solution or its lyophilisate  
 used for diagnosis of cardiac or skeletal muscle damage  
 PS Example 3: Page 67-68; 94PP; English.  
 CC This protein sequence comprises a fusion protein with the  
 N-terminal region being human cardiac troponin I (HcTnI) and  
 CC the C-terminal region being human cardiac troponin C (HcTnC). It  
 has been expressed in E. coli host cells utilising a vector  
 carrying a HcTnI-HcTnC polynucleotide (see V04225) obtained by PCR.  
 The addition of the calcium binding protein HcTnC to HcTnI provided  
 more favourable solubility properties to HcTnI. The invention  
 provides an assay for measuring mammalian, preferably human,  
 troponin in a patient sample. The assay includes the step of  
 comparing the level in the sample with a novel troponin protein  
 standard. This may be a storage stable, soluble mammalian troponin,  
 a functional fragment of the troponin, a modified troponin or its  
 functional fragment, a troponin fusion protein or a heteromultimeric  
 troponin complex (see also W41570-75). The method is used to  
 monitor changes in the level of human troponin, particularly for  
 diagnosis of diseases involving damage to heart or skeletal muscle,  
 e.g. acute myocardial infarction. It may also be used to study  
 CC normal and pathological functions of troponin-expressing tissues.  
 CC Sequence 372 AA;

RESULT 7  
 ID W18053 standard; protein; 153 AA.

AC W18053; 7  
 DT 20-FEB-1998 (first entry)

CC Recombinant myofibrillar contractile protein Troponin I, cTnI; cTnI;  
 CC Cardiac isotype; myofibrillar contractile protein; Troponin I; cTnI;  
 CC inhibitory subunit; thin filament regulatory protein; TnI immunoassay;  
 CC calcium sensitivity; cardiac muscle; striated muscle;  
 CC degradation product; cardiac muscle cleavage; myocardial infarction;  
 CC immunological activity.

OS Homo sapiens.  
 PH Location/Qualifiers  
 FT Modified\_site 79 /note= "carboxymethylated to prevent dimerisation by  
 FT inter or intra disulphide bridges"  
 FT Modified\_site 96 /note= "carboxymethylated to prevent dimerisation by  
 FT inter or intra disulphide bridges"  
 PN W0971955-A1.  
 PD 05-JUN-1997.  
 PF 26-NOV-1995; 018878.  
 PR (DADE) DADE INT INC.  
 PI Demarco C, Moriana NA;  
 DR WB; 91/30526/28.

PT Human cardiac Troponin I cyanogen bromide cleaved fragment - used in  
 PR calibrator or control for troponin I immunoassay  
 Disclosure; Page 20; 52PP; English.  
 PS The present sequence represents a CN-Br cleavage fragment of the  
 CC recombinant cardiac isotype of the myofibrillar contractile protein  
 CC troponin I (cTnI). Troponin I is the inhibitory subunit of Troponin,  
 CC a thin filament regulatory protein complex which confers calcium  
 CC sensitivity to the cardiac and striated muscle. The present 153 amino

CC acid CNBr-cTnI isoform is used in a calibrator or a control for a TnI  
 CC immunoassay. The CNBr-cTnI isoform is comparable in molecular weight to  
 CC a major degradation product of native cTnI in the serum of patients who  
 CC have experienced myocardial infarction. The Peptide has immunological  
 CC activity to antibodies against TnI. The CNBr-cTnI isoform has an average  
 CC of 3-4 times more reactivity than TnI and lower non specific binding, as  
 CC measured by radial partition immunoassay. It also has increased stability  
 CC over the synthetic peptide currently used in the Dade TnI immunoassay.  
 CC Sequence 153 AA;

RESULT 8  
 ID W02286 standard; peptide; 80 AA.  
 AC W02286;  
 DT 27-MAY-1997 (first entry)  
 CC Human troponin I fragment, residues 2-81 (initial Met is residue 1).  
 DE Cardiac heart; troponin I; fragment; analyte; aqueous calibrator;  
 KW stabiliser; myosin; myoglobin; lactate dehydrogenase; creatine kinase;  
 KW myocardial infarction; heart attack.  
 OS Homo sapiens.  
 PN W09627561-A1.  
 PD 12-SEP-1996.  
 PF 06-MAR-1996; 003034.  
 PR 07-MAR-1995; US-000158.  
 PA (DADE) DADE INT INC.  
 PI Bauer R, Chin B, Flaa C, Sabucedo A;  
 DR WPI; 96-425423/42.  
 PT Ag. compsn. for stabilising proteins for use as controls for cardiac  
 PT markers - comprising buffer, reducing agent, stabilising protein,  
 PT chelating agent and salt.  
 AC W1055; 8  
 DT 11-FEB-1998 (first entry)  
 CC W02286 and W02286 are troponin I fragments used to exemplify the  
 CC usefulness of an aqueous composition (may be lyophilised) used as an  
 CC aqueous calibrator and control solution for diagnostic assays for  
 CC cardiac proteins and peptides. The stabilising solution comprises a  
 CC buffer, a reducing agent (e.g. 2-mercaptopropanol or N-acetyl-cysteine),  
 CC a stabilising protein (e.g. albumin or casein), a chelating agent (e.g.  
 CC EDTA or EGTA), a salt (e.g. NaCl), a bulking agent (especially gelatine),  
 CC and a bulking agent (e.g. trehalose, glucose, sucrose, galactose, etc.).  
 CC The composition is especially useful for diagnostic assays of  
 CC troponin, myoglobin, creatine kinase (CK), CK isoenzymes, lactate  
 CC dehydrogenase (LD), LD isoenzymes, myosin and proteins of these. The  
 CC composition may be used, e.g. in tests for acute myocardial infarction.  
 CC The stabilising composition is not derived from human serum, and thus  
 CC prevents exposure of the user (and manufacturing personnel) to many of  
 CC the diseases which can be spread by contact with human blood products.  
 CC The composition is also able to keep analytes stable in liquid form for  
 CC extended periods of time.  
 SQ Sequence 80 AA;

RESULT 8  
 ID W02286 standard; peptide; 80 AA.

AC W1055; 8  
 DT 11-FEB-1998 (first entry)

CC Recombinant myofibrillar contractile protein Troponin I, cTnI; cTnI;  
 CC Cardiac isotype; myofibrillar contractile protein; Troponin I; cTnI;  
 CC inhibitory subunit; thin filament regulatory protein; TnI immunoassay;  
 CC calcium sensitivity; cardiac muscle; striated muscle;  
 CC degradation product; cardiac muscle cleavage; myocardial infarction;  
 CC immunological activity.

OS Homo sapiens.  
 PH Location/Qualifiers  
 FT Modified\_site 79 /note= "carboxymethylated to prevent dimerisation by  
 FT inter or intra disulphide bridges"  
 FT Modified\_site 96 /note= "carboxymethylated to prevent dimerisation by  
 FT inter or intra disulphide bridges"  
 PN W0971955-A1.  
 PD 05-JUN-1997.  
 PF 26-NOV-1995; 018878.  
 PR (DADE) DADE INT INC.  
 PI Demarco C, Moriana NA;  
 DR WB; 91/30526/28.

PT Human cardiac Troponin I cyanogen bromide cleaved fragment - used in  
 PR calibrator or control for troponin I immunoassay  
 Disclosure; Page 20; 52PP; English.  
 PS The present sequence represents a CN-Br cleavage fragment of the  
 CC recombinant cardiac isotype of the myofibrillar contractile protein  
 CC troponin I (cTnI). Troponin I is the inhibitory subunit of Troponin,  
 CC a thin filament regulatory protein complex which confers calcium  
 CC sensitivity to the cardiac and striated muscle. The present 153 amino

CC acid CNBr-cTnI isoform is used in a calibrator or a control for a TnI  
 CC immunoassay. The CNBr-cTnI isoform is comparable in molecular weight to  
 CC a major degradation product of native cTnI in the serum of patients who  
 CC have experienced myocardial infarction. The Peptide has immunological  
 CC activity to antibodies against TnI. The CNBr-cTnI isoform has an average  
 CC of 3-4 times more reactivity than TnI and lower non specific binding, as  
 CC measured by radial partition immunoassay. It also has increased stability  
 CC over the synthetic peptide currently used in the Dade TnI immunoassay.  
 CC Sequence 153 AA;

RESULT 8  
 ID W02286 standard; peptide; 80 AA.

AC W1055; 8  
 DT 11-FEB-1998 (first entry)

CC Recombinant myofibrillar contractile protein Troponin I, cTnI; cTnI;  
 CC Cardiac isotype; myofibrillar contractile protein; Troponin I; cTnI;  
 CC inhibitory subunit; thin filament regulatory protein; TnI immunoassay;  
 CC calcium sensitivity; cardiac muscle; striated muscle;  
 CC degradation product; cardiac muscle cleavage; myocardial infarction;  
 CC immunological activity.

OS Homo sapiens.  
 PH Location/Qualifiers  
 FT Modified\_site 79 /note= "carboxymethylated to prevent dimerisation by  
 FT inter or intra disulphide bridges"  
 FT Modified\_site 96 /note= "carboxymethylated to prevent dimerisation by  
 FT inter or intra disulphide bridges"  
 PN W0971955-A1.  
 PD 05-JUN-1997.  
 PF 26-NOV-1995; 018878.  
 PR (DADE) DADE INT INC.  
 PI Demarco C, Moriana NA;  
 DR WB; 91/30526/28.

PT Human cardiac Troponin I cyanogen bromide cleaved fragment - used in  
 PR calibrator or control for troponin I immunoassay  
 Disclosure; Page 20; 52PP; English.  
 PS The present sequence represents a CN-Br cleavage fragment of the  
 CC recombinant cardiac isotype of the myofibrillar contractile protein  
 CC troponin I (cTnI). Troponin I is the inhibitory subunit of Troponin,  
 CC a thin filament regulatory protein complex which confers calcium  
 CC sensitivity to the cardiac and striated muscle. The present 153 amino

CC acid CNBr-cTnI isoform is used in a calibrator or a control for a TnI  
 CC immunoassay. The CNBr-cTnI isoform is comparable in molecular weight to  
 CC a major degradation product of native cTnI in the serum of patients who  
 CC have experienced myocardial infarction. The Peptide has immunological  
 CC activity to antibodies against TnI. The CNBr-cTnI isoform has an average  
 CC of 3-4 times more reactivity than TnI and lower non specific binding, as  
 CC measured by radial partition immunoassay. It also has increased stability  
 CC over the synthetic peptide currently used in the Dade TnI immunoassay.  
 CC Sequence 153 AA;

RESULT 8  
 ID W02286 standard; peptide; 80 AA.

AC W1055; 8  
 DT 11-FEB-1998 (first entry)

CC Recombinant myofibrillar contractile protein Troponin I, cTnI; cTnI;  
 CC Cardiac isotype; myofibrillar contractile protein; Troponin I; cTnI;  
 CC inhibitory subunit; thin filament regulatory protein; TnI immunoassay;  
 CC calcium sensitivity; cardiac muscle; striated muscle;  
 CC degradation product; cardiac muscle cleavage; myocardial infarction;  
 CC immunological activity.

OS Homo sapiens.  
 PH Location/Qualifiers  
 FT Modified\_site 79 /note= "carboxymethylated to prevent dimerisation by  
 FT inter or intra disulphide bridges"  
 FT Modified\_site 96 /note= "carboxymethylated to prevent dimerisation by  
 FT inter or intra disulphide bridges"  
 PN W0971955-A1.  
 PD 05-JUN-1997.  
 PF 26-NOV-1995; 018878.  
 PR (DADE) DADE INT INC.  
 PI Demarco C, Moriana NA;  
 DR WB; 91/30526/28.

PT Human cardiac Troponin I cyanogen bromide cleaved fragment - used in  
 PR calibrator or control for troponin I immunoassay  
 Disclosure; Page 20; 52PP; English.  
 PS The present sequence represents a CN-Br cleavage fragment of the  
 CC recombinant cardiac isotype of the myofibrillar contractile protein  
 CC troponin I (cTnI). Troponin I is the inhibitory subunit of Troponin,  
 CC a thin filament regulatory protein complex which confers calcium  
 CC sensitivity to the cardiac and striated muscle. The present 153 amino

RESULT	9	the diseases which can be spread by contact with human blood products.
ID	R66181 standard; peptide: 38 AA.	CC The composition is also able to keep analytes stable in liquid form for extended periods of time.
AC	R66181	CC
DR	21-JUL-1995 (first entry)	CC
DE	Cardiac troponin I peptide fragment #1.	Query Match 34.2%; Score 233; DB 21; Length 35;
KW	Cardiac troponin I; skeletal troponin I; immunoassay; antibody; myocardial damage; myocardial infarction.	Best Local Similarity 100.0%; Pred. No. 7.62e-12;
KW	Synthetic.	Mismatches 0; Indels 0; Gaps 0;
OS		
PN	W09427156-A.	
PD	24-NOV-1994.	
PR	16-MAY-1994; U05468.	
PR	17-MAY-1993; US-063168.	
PA	(FORT-) FORTRON BIOSCIENCE INC.	RESULT 11
PI	Torretti SA, Vargas AM, Wicks RW, Zartman LO;	ID W37924 standard; peptide: 31 AA.
DR	WPI: 95-006373/01.	AC W37924;
PR	Quantitative assay of cardiac troponin I - for diagnosis of myocardial damage, esp. infarction, also new antibodies specific for cardiac but not skeletal troponin I.	DT 09-SEP-1998 (first entry)
PT	PS	DE N-terminal amino acid sequence of cardiac troponin I.
PT	CC	KW Cardiac troponin I; cTnI; acute myocardial infarction; inhibition; Cardio troponin I; cTnI; cardio-specific marker.
PS	CC	KW Homo sapiens.
CC	CC	PN W0916255-A2.
CC	CC	PD 23-APR-1998.
CC	CC	PT 15-OCT-1997; U18368.
CC	CC	PR 15-OCT-1997; US-730111.
CC	CC	PR 15-OCT-1996; US-730111.
CC	CC	PA (NAVI-) NAVIX INC.
CC	CC	PI Botyanszki J, Dave KT, Sintar E;
CC	CC	DR WPI: 98-251059/22.
CC	CC	PT Stabilising individual sub-units of multimeric protein by attaching to polymer - particularly cardiac troponin sub-units for use as controls in immunoassays for diagnosis of acute myocardial infarction
CC	CC	PT controls in immunoassays for diagnosis of acute myocardial infarction
CC	CC	PS Disclosure; Page 14; 34pp; English.
CC	CC	This is the amino acid sequence of the N-terminal sequence of the cardiac troponin I (cTnI) protein, acts as an inhibitory subunit to cardiac troponin T (cTnT), which is released after an acute myocardial infarction. The cTnI and cTnT are useful as cardio-specific markers. Particularly for early diagnosis of acute myocardial infarction by immunoassays. The stabilised subunits are used as control reagents in such assays.
CC	CC	RESULT 10
CC	CC	ID W02285 standard; peptide: 35 AA.
AC	AC	AC W02285;
DR	27-MAY-1997 (first entry)	Query Match 30.4%; Score 207; DB 32; Length 31;
DE	Human troponin I fragment, residues 27-61 (initial Met is residue 1).	Best Local Similarity 100.0%; Pred. No. 1.73e-09;
KW	Cardiac heart; troponin I; fragment; analyte; aqueous calibrator;	Mismatches 0; Indels 0; Gaps 0;
KW	stabiliser: myosin; myoglobin; lactate dehydrogenase; creatine kinase;	
KW	myocardial infarction; heart attack.	
OS	Homo sapiens.	
PN	W09627261-A1.	
PD	12-SEP-1996.	
PR	06-MAR-1996; U03034.	
PR	07-MAR-1995; U-400158.	
PA	(DADE) DADE INT INC.	RESULT 12
PI	Bauer, Chin B, Flaa C, Sabucedo A;	ID R55781 standard; peptide: 30 AA.
DR	WPI: 96-425423/42.	AC R55781;
PT	Ag. compsn. for stabilising proteins for use as controls for cardiac markers - comprising buffer, reducing agent, stabilising protein, PT chelating agent and salt.	DT 21-FEB-1995 (first entry)
PT	PS	DE Human cardiac troponin I N-terminal sequence.
PT	CC	KW Human cardiac troponin I; heart muscle necrosis; immunogen; epítope; immunodiagnosis; acute myocardial infarction.
CC	CC	KW Homo sapiens.
CC	CC	PN DE4243648-A.
CC	CC	PD 07-JUL-1994.
CC	CC	PR 23-DEC-1992; DE-243648-B.
CC	CC	PA (BOEING) BOEING MANNHEIM GMBH.
CC	CC	PI Borgya A, Donie F, Lill H, Seidel C;
CC	CC	DR WPI: 94-218764/27.
CC	CC	PT Rapid diagnosis of heart muscle necrosis in myocardial infarction by immunological test using new antibody recognising cardiac troponin 1 N-terminal peptide.
CC	CC	PT troponin 1 N-terminal peptide.
CC	CC	PS Clapp I; Page 8; 12pp; German.
CC	CC	The N-terminal 30 amino acids of human cardiac troponin I (R55781) or subfragments of it (R55782-R55788) can be used as immunogens. The
CC	CC	CC

CA213280-A.  
 PN 25-FEB-1995.  
 PD 17-AUG-1994; 130280.  
 PR 24-AUG-1993; US-110824.  
 (SPEC-) SPECTRAL DIAGNOSTICS INC.  
 PA Jackowski G, Lee L;  
 WPI: 95-155575/21.  
 DR New intact cardiac troponin I from heart tissue - isolated in  
 presence of urea and protease inhibitors, useful as calibrator and  
 quality control standard for troponin assay.  
 PT quality control standard for troponin assay.  
 PPT quality control standard for troponin assay.  
 PPS Claim 8; Page 6; 30pp; English.  
 The sequence shown is the N-terminal sequence of cardiac troponin  
 (cTnI). This sequence was used in the development of a method for  
 purifying cardiac troponin I with increased stability. The method  
 to extract the cTnI in the presence of a mixture of protease inhibitor  
 this mixture of protease inhibitors includes at least 2 cathepsin  
 protease inhibitors, at least 1 serine protease inhibitor and at 1  
 1 cysteine protease inhibitor. This mixture is effective to inhibit  
 degradation of the cardiac specific N-terminal region of cTnI, whi  
 this sequence. The advantage of this method is that it enables  
 practically intact cTnI that has good storage stability to be isol  
 The cTnI may then be used as a sensitive early indicator of myocar  
 infarction.  
 Sequence 31 AA;  
 SQ 29.68; Score 202; DB 14; Length 31;  
 Best Local Similarity 100.0%; Prod. No. 4.88e-09;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gap 0  
 Db 1 adgssdaarenrpapapirrrssnyrayate 31  
 Qy 2 ADGSSDAAREPAPAPIRRRSSNYRAYATE 32

PS Claim 8; Column 13:14; 12PP; English.  
CC This sequence represents the N-terminus of human cardiac troponin I. The  
CC degradation of this sequence is inhibited by the protease inhibitor  
CC mixture used in the method of the invention. The method of the invention  
CC is for isolating a pure, stable cardiac troponin I preparation, where the  
CC troponin I has a molecular weight of about 28 kDa. The method comprises  
CC extracting human cardiac tissue with an aqueous extraction buffer at a pH  
CC of 7 to 9 which is 8 to 10 M in urea and contains a protease inhibitor  
CC mixture. The troponin I is then separated from the extract by affinity  
CC chromatography in the presence of the extraction buffer and calcium ions  
CC thereby to absorb the troponin I. The troponin I is then desorbed by  
CC washing with the aqueous extraction buffer containing EGTA. The protease  
CC inhibitor mixture used comprises at least two cathepsin protease  
CC inhibitors, at least one serine protease inhibitor and at least one  
CC cysteine protease inhibitor. The inhibitor mixture may also contain an  
CC aspartate protease inhibitor, an aminopeptidase protease inhibitor and  
CC a metalloendopeptidase inhibitor. The isolated troponin I can be used as  
CC a standard in detection assays for early detection of myocardial  
CC infarction. The method provides pure and stable troponin which can  
CC provide for reproducible and reliable clinical testing.

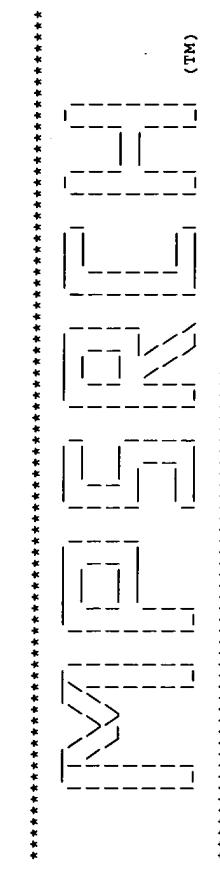
**RESULT** 14  
 ID R73052 standard; peptide: 31 AA.  
 AC R73022;  
 DT 14-DEC-1995 (first entry)  
 DE N-terminal sequence of cardiac troponin I.  
 KW Cardiac troponin I; ctnI; N-terminal region; cardiac specific;  
 KW protease inhibitor; myocardial infarction.  
 KW Homo sapiens.

CC angiofibroma, atherosclerotic plaques, delayed wound healing, CC granulations, haemophilic joints, hypertrophic scars, nonunion CC fractures, Osler-Weber syndrome, pyogenic granuloma, scleroderma, CC trachoma, and vascular adhesions.  
Sequence 182 AA;

Query	Match	29.5%	Score	201;	DB	26;	Length	182;
Best Local Matches	Local Similarity	39.7%	Prod. No.	5.99e-09;				
25;	Conservative	21;	Mismatches	16;	Indels	1;	Gaps	1;
Db	6	krnraitarzchlkwmlqiaatelekesrreakeqnylaehcpcphlhipg-simsevgel	64					
Qy	37	KKSKEIASRKQLQLKLTLLQIAKQELEREAAERRGEKGKRALSTRCQPLLEAGLGFAELQDL	96					
Db	65	ckq	67					
Qv	97	CRO	99					

Search completed: Fri Jan 21 14:31:17 2000  
Job time : 60 secs.

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MSrch\_pp

protein - protein database search, using Smith-Waterman algorithm

Run on:

Fri Jan 21 14:29:29 2000;

MasPar time 6.59 Seconds

602.084 Million cell updates/sec

Tabular output not generated.

Title: >US-09-176-546-2  
 Description: (1-99) from US09176546.pep  
 Perfect Score: 682  
 Sequence: 1 MADGSSDAAREPRPAPAPIR.....COPPLELAGLGFAEIQLICRQ 99

Scoring table: PAM 150

Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Pir60

1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 40.178; Variance 87.144; scale 0.461W

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	Pred. No.
1	682	100.0	210	1 TPUIC	1.31e-103
2	614	90.0	211	2 A55805	8.63e-91
3	610	89.4	211	2 A60124	4.87e-89
4	608	89.1	211	2 I56441	1.16e-89
5	592	86.8	216	1 TPPBIC	1.16e-86
6	586	85.9	211	2 A29994	1.54e-85
7	431	63.2	208	2 A41030	7.90e-57
8	429	62.9	244	2 I51408	1.83e-56
9	237	34.8	187	2 B44786	1.68e-22
10	231	33.9	187	1 TPUIC	1.72e-21
11	219	32.1	184	1 TPPBIC	1.72e-19
12	210	30.8	142	2 JC5611	5.28e-18
13	209	30.6	142	2 A41030	7.70e-18
14	208	30.5	182	1 TPPBIS	1.12e-17
15	205	30.1	182	2 A44786	3.49e-17
16	201	29.5	182	1 TPUIC	1.57e-16
17	193	28.3	173	2 JC5610	3.11e-15
18	192	28.2	183	2 A29569	4.50e-15
19	192	28.2	183	1 TPPBIS	4.50e-15
20	152	22.3	176	2 S70008	8.18e-09
21	144	21.1	208	2 A40547	1.29e-07
22	143	21.0	260	2 B31594	1.82e-07
23	136	19.9	201	2 A31484	1.93e-06

## ALIGNMENTS

RESULT	ENTRY	TPUIC	*type complete
	TITLE	#formal_name Homo sapiens #common_name man	
	ORGANISM	03-May-1994 #sequence_revision 03-May-1996 #text_change	
	DATE	05-Sep-1997	
	ACCESSIONS		
	REFERENCE	AG1229; JN0837; S11522; A33185; S63690	
	authors	Hankeler, N.M.; Kullman, J.; Murphy, A.M.	
	journal	Circ. Res. (1991) 69:1409-1414	
	#cross-references	Troponin I isoform expression in human heart. MUID:92035427	
	accession	AG1229	
	#status	##not compared with conceptual translation	
	#molecule-type	mRNA	
	RESIDUES	JN0837	
	authors	Armour, K.L.; Harris, W.J.; Tempest, P.R.	
	journal	Gene (1993) 131:287-312	
	#title	Cloning and expression in Escherichia coli of the cDNA encoding human cardiac troponin I.	
	#cross-references	MUID:94010323	
	accession	JN0837	
	#molecule-type	mRNA	
	#residues	1-210 ##label AR2	
	#cross-references	GB:MG4247; NID:9339966; PID:9339967	
	REFERENCE	S11522	
	authors	Vallins, W.J.; Brand, N.J.; Butler-Browne, G.; Yacoub, M.H.; Barton, P.J.R.	
	journal	FEBS Lett. (1990) 270:57-61	
	#title	Molecular cloning of human cardiac troponin I using polymerase chain reaction.	
	#cross-references	MUID:91032031	
	accession	S11522	
	#molecule-type	mRNA	
	#residues	1-85, 'T', 87-210 ##label VAL	
	#cross-references	EMBL:X54163; NID:97427; PID:937428	
	REFERENCE	S11886	
	authors	Mittmann, K.; Jaquet, K.; Heilmeyer Jr., L.M.G.	
	journal	FEBS Lett. (1990) 273:41-45	
	#title	A common motif of two adjacent phosphosertines in bovine, rabbit and human cardiac troponin I.	
	#cross-references	MUID:91032199	
	#contents	annotation; acetylated amino end; phosphorylation sites	
	#gene	GDB:TNNI3	
	#cross-references	GDB:1253039; OMIM:191044	

#map\_position 19p13.2-19q13.2  
troponin is a heterotrimer with one molecule each of troponin C (calcium binding component) troponin I (inhibitory component), and troponin T (tropomyosin-binding component)

**FUNCTION**

**#description** binds actin and inhibits myosin ATPase activity; with tropomyosin mediates contraction of vertebrate striated muscle in response to calcium

**#pathway**

**CLASSIFICATION**

**KEYWORDS**

**FEATURE**

2 23, 24

**SUMMARY**

Query Match 100.0% Score 682; DB 1; Length 210;  
Best Local Similarity 100%; Pred. No. 1.31e-103; Gaps 0;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MADGSSDAAREPPAPAPIRRSSNYRAYATEPHAKKSISASRKQLQKTLQIAKQ 60  
QY 1 MADGSSDAAREPPAPAPIRRSSNYRAYATEPHAKKSISASRKQLQKTLQIAKQ 60

Db 61 LEREAERGERGEKRALSTRCQPLELAGLGFATQDLCRQ 99  
QY 61 LEREAERGERGEKRALSTRCQPLELAGLGFATQDLCRQ 99

**RESULT**

2 A53805 #type complete  
troponin I, cardiac - mouse  
#formal\_name Mus musculus #common\_name house mouse  
DATE 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change  
17-Mar-1999

ACCESSIONS  
REFERENCE A53805; A53108

ENTRY #authors Guo, X.; Wattanapenpools, J.; Palmiter, K.A.; Murphy, A.M.; Solano, R.J.

TITLE #journal J. Biol. Chem. (1994) 269:15210-15216

ORGANISM #title Mutagenesis of cardiac troponin I. Role of the unique NH<sub>2</sub>-terminal peptide in myofilament activation.

DATE #cross-references MUID:94253083

#status A53805  
#molecule\_type mRNA  
#residues preliminary  
##CROSS REFERENCES GB:U09181; NID:9484093; PID:9508866

REFERENCE #authors Ausoni, S.; Campione, M.; Picard, A.; Moretti, P.; Vitadello, M.; De Nardi, C.; Schiaffino, S.

#journal J. Biol. Chem. (1994) 269:339-346

#title Structure and regulation of the mouse cardiac troponin I gene

#cross-references MUID:94103333

ACCESSIONS A53108

#status preliminary; translated from GB/EMBL/DDJB

#molecule\_type DNA  
#residues 1-111 #label RES

#cross-references EMBL:Z2274; NID:9313104; PID:9313105

GENETICS #introns 4/2; 8/3; 51/3; 95/3; 125/3; 184/3

CLASSIFICATION #superfamily troponin I  
KEYWORDS actin binding; heart; phosphoprotein  
SUMMARY #length 211 #molecular\_weight 24259 #checksum 7181

Query Match 90.0% Score 614; DB 2; Length 211;  
Best Local Similarity 89.0%; Pred. No. 8.63e-91; Gaps 1; Gaps 1;  
Matches 89; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Db 1 MADESSDAAGEQPAPAPVRRSSNYRAYATEPHAKKSISASRKQLQKTLQIAKQ 60  
QY 1 MADGSSDAAREPPAPAPIRRSS-NRAYATEPHAKKSISASRKQLQKTLQIAKQ 59

**RESULT**

3 A60124 #type complete  
troponin I, cardiac muscle - rat  
#formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change  
31-Oct-1997

ACCESSIONS A60124; A60124

REFERENCE A60124

#authors Ausoni, S.; De Nardi, C.; Moretti, P.; Gorza, L.; Schiaffino, S.

#journal Development (1991) 112:1041-1051

#title Developmental expression of rat cardiac troponin I mRNA.  
#accession A60124

#molecule\_type mRNA  
#residues 1-211 #label AUS

#cross-references EMBL:X5849; NID:956022; PID:956023

REFERENCE A33398

#authors Murphy, A.M.; Jones II, L.; Sims, H.F.; Strauss, A.W.

#journal Biochemistry (1991) 30:707-712

#title Molecular cloning of rat cardiac troponin I and analysis of troponin I isoform expression in developing rat heart.  
#cross-references MUID:91105162

#accession A33398

#molecule\_type mRNA  
#residues 1-211 #label MUR

#cross-references GB:M7679; GB:J-05304; NID:9207509; PID:9207510

CLASSIFICATION #superfamily troponin I  
KEYWORDS actin binding; cardiac muscle; heart  
SUMMARY #length 211 #molecular\_weight 24159 #checksum 7678

Query Match 89.4% Score 610; DB 2; Length 211;  
Best Local Similarity 89.0%; Pred. No. 4.7e-90; Gaps 1; Gaps 1;  
Matches 89; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Db 1 MADESSDAAGEQPAPAPVRRSSNYRAYATEPHAKKSISASRKQLQKTLQIAKQ 60  
QY 1 MADGSSDAAREPPAPAPIRRSS-NRAYATEPHAKKSISASRKQLQKTLQIAKQ 59

**RESULT**

4 156441 #type complete  
troponin I - rat  
#formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change  
23-Feb-1997

ACCESSIONS 156441

REFERENCE 156441

#authors Martin, A.F.; Orlowski, J.

#journal J. Mol. Cell. Cardiol. (1991) 23:583-588

#title Molecular cloning and developmental expression of the rat cardiac-specific isoform of troponin I.

#cross-references MUID:9135915

ACCESSIONS 156441

REFERENCE 156441

#status preliminary; translated from GB/EMBL/DDJB

#molecule\_type mRNA  
#residues 1-211 #label RES

#cross-references GB:M9207515; NID:9207516

CLASSIFICATION #superfamily troponin I  
SUMMARY #length 211 #molecular\_weight 24163 #checksum 7943

Query Match 90.0% Score 614; DB 2; Length 211;  
Best Local Similarity 89.0%; Pred. No. 8.63e-91; Gaps 1; Gaps 1;  
Matches 89; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Query Match 89.1%; Score 608; DB 2; Length 211;  
Best Local Similarity 88.0%; Pred. No. 1.16e-89;  
Matches 88; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

D<sub>b</sub> 1 MADDESSDAGEPAPAPVRRSSANRYAYATEPHAKKSISASRKQLQTKLMLQIAKQ 60  
Q<sub>y</sub> 1 MADSSDAREPAPAPAPIRSS\_NYRAYATEPHAKKSISASRKQLQTKLMLQIAKQ 59

D<sub>b</sub> 61 EMEREAERGERGEKGRVSLSTRCQPLYLDGLGFEELQDLCRQ 100  
Q<sub>y</sub> 60 EMEREAERGERGEKGRVSLSTRCQPLYLDGLGFEELQDLCRQ 99

RESULT 5 TPRBIC #type complete  
ENTRY ENTRY  
TITLE TITLE  
ORGANISM ORGANISM  
DATE DATE  
ACCESSIONS ACCESSIONS  
REFERENCE REFERENCE  
#authors #authors  
#journal #journal  
#title #title  
#cross-references #cross-references  
#accession #accession  
#molecule-type #molecule-type protein  
#residues #residues  
#cross-references #cross-references MUID:78060292  
#accession #accession A90294  
#molecule-type protein  
#residues 1-4,'R',6-16,18-20,22,'D',27-211 #label GRA  
REFERENCE S12886  
#authors Mittmann, K.; Jaquet, K.; Heilmeyer Jr., L.M.G.  
#journal FEBS Lett. (1990) 273:41-45  
#title A common motif of two adjacent phosphoserines in bovine,  
rabbit and human cardiac troponin I.  
#cross-references MUID:77087072  
#accession S12886  
#molecule-type protein  
#residues 1-36 #label MIT  
#note peptide sequences corrected; amino terminal acetylation;  
#cross-references MUID:91032199  
#accession S12886  
#molecule-type protein  
#residues 1-36 #label MIT  
#note peptide sequences corrected; amino terminal acetylation;  
#cross-references MUID:91032199  
#accession S12886  
#molecule-type protein  
#residues 1-36 #label MIT  
#note peptide sequences corrected; amino terminal acetylation;  
#cross-references MUID:91032199  
#accession S12886  
#molecule-type protein  
#residues 1-36 #label MIT  
#note peptide sequences corrected; amino terminal acetylation;

REFERENCE A93181  
#authors Solaro, R.J.; Moir, A.J.G.; Perry, S.V.  
#title Nature (1976) 262:615-617  
#cross-references MUID:76367707  
#contents COMPLEX  
#FUNCTION #description  
#pathway  
#CLASSIFICATION  
#KEYWORDS  
#FEATURE 1  
#FEATURE 22, 23  
#SUMMARY

Query Match 86.8%; Score 592; DB 1; Length 216;  
Best Local Similarity 89.9%; Pred. No. 1.16e-86;  
Matches 89; Conservative 4; Mismatches 4; Indels 2; Gaps 2;

D<sub>b</sub> 1 ADESTDAEPRAPAPVRRSSANRYAYATEPHAKSKKK\*ISASRKQLQTKLMLQIAKQ 60  
Q<sub>y</sub> 2 ADSSDAREPAPAPIRSS\_NYRAYATEPHAKSKR\*ISASRKQLQTKLMLQIAKQ 59

D<sub>b</sub> 61 ELEERAERGERGEKGRVSLSTRCQPLELAGLGFAELQDLCRQ 99  
Q<sub>y</sub> 60 ELEERAERGERGEKGRVSLSTRCQPLELAGLGFAELQDLCRQ 98

RESULT 6 A29994 #type complete  
ENTRY ENTRY  
TITLE TITLE  
ORGANISM ORGANISM  
DATE DATE  
ACCESSIONS ACCESSIONS  
REFERENCE REFERENCE  
#authors Leszzyk, J.; Dumaswala, R.; Potter, J.D.; Collins, J.H.  
#journal Biochemistry (1988) 27:2821-2827  
#title Amino acid sequence of bovine cardiac troponin I.  
#cross-references MUID:88294022  
#accession A29994  
#molecule-type protein  
#residues 1-211 #label LES  
REFERENCE S02628  
#authors Swiderk, K.; Jaquet, K.; Meyer, H.E.; Heilmeyer Jr., L.M.G.  
#journal Bur. J. Biochem. (1988) 176:335-342  
#title Cardiac troponin I, isolated from bovine heart, contains two  
adjacent phosphoserines. A first example of phosphoserine  
determination by derivatization to S-ethylcysteine.  
#cross-references MUID:88329087  
#accession S02628  
#molecule-type protein  
#residues 21-27, 'Y', 28-37 #label SWI  
#note authors comment in a note added in proof that the extra  
tyrosine is an error  
CLASSIFICATION #superfamily troponin I  
#KEYWORDS acetylated amino end; actin binding; cardiac muscle; heart;  
#FEATURE 1 #modified-site acetylated amino end (Ala) #status  
#experimental #binding-site phosphate (Ser) (covalent) #status  
#SUMMARY #length 211 #molecular-weight 23922 #checksum 5928

Query Match 85.9%; Score 586; DB 2; Length 211;  
Best Local Similarity 88.7%; Pred. No. 1.54e-85;  
Matches 86; Conservative 6; Mismatches 3; Indels 2; Gaps 2;

D<sub>b</sub> 5 GGSTG-DIVPAPPVRRSSANRYAYATEPHAKSKKISASRKQLQTKLMLQIAKQLE 63  
Q<sub>y</sub> 4 GSSDAAREPAPAPIRSS\_NYRAYATEPHAKSKKISASRKQLQTKLMLQIAKQLE 62

D<sub>b</sub> 64 REAEERGERGEKGRVSLSTRCQPLELAGLGFAELQDLCRQ 100  
Q<sub>y</sub> 63 REAEERGERGEKGRVSLSTRCQPLELAGLGFAELQDLCRQ 99

RESULT 7 A41030 #type complete  
ENTRY ENTRY  
TITLE TITLE  
ORGANISM ORGANISM  
DATE DATE  
ACCESSIONS ACCESSIONS  
REFERENCE A41030  
#authors Shimada, Y.; Toyota, N.; Hatings, K.E.M.; Koppe, R.I.; Marmor, E.; Bader, D.;



SUMMARY #length 187 #molecular-weight 21692 #checksum 7017

Query Match 33.9%; Score 231; DB 1; Length 187;  
Best Local Similarity 50.7%; Pred. No. 1.72e-21; Indels 0; Gaps 0;  
Matches 34; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Db 2 PEVERKPKITASRKULLKSLMALKAKECWQEHREAAKVRYLAAERIPLQLTRGLSLSA 61  
Qy 33 PHAKKSISRKQLQKTLQIAKQELREAAERGEGRALSTRCOPLEAGLGFAE 92

Db 62 LQDLCRE 68  
Qy 93 LQDLCRQ 99

RESULT 11 TPRBIW #type complete  
ENTRY troponin I, slow skeletal muscle - rabbit  
ORGANISM #formal\_name Oryctolagus cuniculus #common\_name domestic  
DATE 30-Apr-1979 #sequence\_revision 30-Apr-1979 #text\_change  
03-May-1996

ACCESSIONS A03089  
REFERENCE A90396  
#authors Grand, R.J.A.; Wilkinson, J.M.  
#title Biochem. J. (1977) 167:183-192  
The amino acid sequence of rabbit slow-muscle troponin I.  
#cross-references MUID:78050292

#molecule\_type Protein  
#residues 1-184 #label GRA  
#note some of the molecules lack residues 183 and 184  
COMPLEX #accession A03089  
#cross-references MUID:98021076

FUNCTION binds actin and inhibits myosin ATPase activity; with  
#pathway troponin mediates contraction of vertebrate striated  
#keywords muscle contraction  
#complex\_name troponin I (inhibitory component), troponin I (troponin-binding component), and troponin T (troponin-T)

FEATURE 1 #modified\_site blocked amino end (Pro) (partial)  
(probably acetylated) #status experimental  
SUMMARY #length 184 #molecular-weight 21143 #checksum 4497

Query Match 32.1%; Score 219; DB 1; Length 184;  
Best Local Similarity 52.2%; Pred. No. 1.72e-19;  
Matches 35; Conservative 13; Mismatches 17; Indels 2; Gaps 2;

Db 1 PEVERKPKITASRKULLKSLMALKAKECWQEHREAAKVRYLAAERIPLQLTRGLSLSA 58  
Qy 33 PHAKKSISRKQLQKTLQIAKQELREAAERGEGRALSTRCOPLEAGLGFAE 92

Db 59 LQDLCRE 65  
Qy 93 LQDLCRQ 99

RESULT 12 JC5611 #type complete  
ENTRY troponin I alpha - sea squirt (Halocynthia roretzii)  
TITLE #formal\_name Halocynthia roretzii  
ORGANISM 23-Sep-1997 #sequence\_revision 17-Oct-1997 #text\_change  
DATE 17-Mar-1999  
ACCESSIONS JC5611  
REFERENCE #authors Yuasa, H.J.; Sato, S.; Yamamoto, H.; Takagi, T.  
#journal J. Biochem. (1997) 122:374-380  
#title Primary structure of troponin I isoforms from the ascidian  
Halocynthia roretzii  
#cross-references MUID:98021076

#accession JC5611  
#molecule\_type mRNA  
##residues 1-142 #label YUA  
#cross-references DDBJ:AB001686; PID:d1020179;  
PID:91888346; PID:91888347

COMMENT This protein binds to actin, and inhibits the interaction between  
actin and myosin. It also binds to troponin C and T.  
CLASSIFICATION #superfamily troponin I  
SUMMARY #length 142 #molecular-weight 16883 #checksum 1681

Query Match 30.6%; Score 210; DB 2; Length 142;  
Best Local Similarity 46.4%; Pred. No. 5.28e-18;  
Matches 26; Conservative 17; Mismatches 12; Indels 1; Gaps 1;

Db 5 RKLQLKSLLNRAREDLKREEQAKEEKKLILNNRLESGLDLSNSQELMELCRE 60  
Qy 45 RKLQLKTLQIAKQELREAAERGEGRALSTRCOPLEAGLGFAEQLDLCRQ 99

RESULT 13 JC5612 #type complete  
ENTRY troponin I beta - sea squirt (Halocynthia roretzii)  
TITLE #formal\_name Halocynthia roretzii  
ORGANISM 23-Sep-1997 #sequence\_revision 17-Oct-1997 #text\_change  
DATE 17-Mar-1999

ACCESSIONS JC5612  
REFERENCE JC5610  
#authors Yuasa, H.J.; Sato, S.; Yamamoto, H.; Takagi, T.  
#journal J. Biochem. (1997) 122:374-380  
#title Primary structure of troponin I isoforms from the ascidian  
Halocynthia roretzii  
#cross-references MUID:98021076

#accession JC5612  
#molecule\_type mRNA  
##residues 1-142 #label YUA  
#cross-references DDBJ:AB001687; PID:91888348; PID:d1020180;  
PID:91888349

COMMENT This protein binds to actin, and inhibits the interaction between  
actin and myosin. It also binds to troponin C and T.  
CLASSIFICATION #superfamily troponin I  
SUMMARY #length 142 #molecular-weight 16840 #checksum 701

Query Match 30.6%; Score 209; DB 2; Length 142;  
Best Local Similarity 48.2%; Pred. No. 7.70e-18;  
Matches 27; Conservative 15; Mismatches 13; Indels 1; Gaps 1;

Db 5 RKLQLKSLLNRAREDLKREEQAKEEKKLILNNRLESGLDLSNSQELMELCRE 60  
Qy 45 RKLQLKTLQIAKQELREAAERGEGRALSTRCOPLEAGLGFAEQLDLCRQ 99

RESULT 14 TPRBIS #type complete  
ENTRY troponin I, fast skeletal muscle - rabbit  
TITLE #formal\_name Oryctolagus cuniculus #common\_name domestic  
ORGANISM #name TNI  
#cross-references A45060; A93193; A90286; I46514; A03087  
#authors Sheng, Z.; Pan, B.S.; Miller, T.E.; Potter, J.D.  
#journal J. Biol. Chem. (1992) 267:25407-25413  
#title Isolation, expression, and mutation of a rabbit skeletal  
muscle cDNA clone for troponin I. The role of the NH2  
terminus of fast skeletal muscle troponin I in its  
biological activity.

#cross-references MUID:93034259  
#accession A45060  
#molecule\_type mRNA  
##residues 1-46, 'DS', 49-182 ##label SHE

```

##cross-references GB:104347
##experimental_source skeletal muscle
##note sequence extracted from NCBI backbone (NCBIP:120236) and
corrected to correspond with the published sequence
##note the authors translated the codons GCC for residue 56 as
Gln, and TAT for residue 80 as Thr

REFERENCE A93193
#authors Wilkison, J.M.; Grand, R.J.A.
#journal Nature (1978) 271:31-35
#title Comparison of amino acid sequence of troponin I from
different striated muscles.

##cross-references MUID:78114026
#accession A93193
#molecule_type protein
##residues 2-154,158-182 ##label WIL

REFERENCE A90286
#authors Wilkison, J.M.; Grand, R.J.A.
#journal Biochem. J. (1975) 144:493-496
#title The amino acid sequence of troponin I from rabbit skeletal
muscle.

##cross-references MUID:76039510
#accession A90286
#molecule_type protein
##residues 2-114,'R',115-154,158-182 ##label WIL2
#cross-references A91408
#authors Noir, A.J.G.; Wilkison, J.M.; Perry, S.V.
#journal FEBS Lett. (1974) 42:53-256
#title The phosphorylation sites of troponin I from white skeletal
muscle of the rabbit.

##cross-references MUID:74309023
#contents annotation: phosphorylation sites
#cross-references A91407
#authors Huang, T.S.; Bylund, D.B.; Stull, J.T.; Krebs, E.G.
#journal FEBS Lett. (1974) 2:249-252
#title The amino acid sequences of the phosphorylated sites in
troponin I from rabbit skeletal muscle.

##cross-references MUID:74306154
#contents annotation: phosphorylation sites
#cross-references I46471
#authors Putney, S.D.; Herlihy, W.C.; Schimmel, P.
#journal Nature (1983) 302:718-721
#title A new troponin T and cDNA clones for 13 different muscle
proteins, found by shotgun sequencing.

##cross-references MUID:83167564
#accession I46514
#status preliminary; translated from GB/EMBL/DBJ
##residues 166-178 ##label PUT
##molecule-type mRNA
##cross-references EMBL:V00898; NID:91738; PID:9229767
#COMPLEX troponin is a heterotrimer with one molecule each of troponin
C (calcium binding component), troponin I (inhibitory
component), and troponin T (tropomyosin-binding component)

#FUNCTION #description binds actin and inhibits myosin ATPase activity; with
tropomyosin mediates contraction of vertebrate striated
muscle in response to calcium
#pathway muscle contraction
#CLASSIFICATION #superfamily troponin I
#KEYWORDS acetylated amino end; actin binding; muscle contraction;
phosphoprotein; skeletal muscle

#FEATURE 2 #modified_site acetylated amino end (Gly) (in mature
#status experimental) form) #status experimental
#binding_site phosphate (Thr) (covalent) (by
#CAMP-dependent kinase) #status experimental \
#binding_site phosphate (Ser) (covalent) (by
#CAMP-dependent kinase) #status experimental
#length 182 #molecular weight 21214 #checksum 8861

Query Match 30.5% Score 208; DB 1; Length 182;
Best Local Similarity 42.9%; Pred. No. 1.12e-17;
Matches 27; Conservative 19; Mismatches 16; Gaps 1;
Indels 1; Gaps 1;
Db 6 KRNRAITRQHLSVMLQIAATELEKERRQRAEAKQNYLAECPPPLPG-SMAEVQEL 64
QY 37 KKSLSASRKQLQLKTLQIAKQELERAAERGEKGRLSTRCQPLAIGFAELQDL 96
Db 65 CKQ 67
QY 97 CRQ 99

RESULT 15 A44786 #type complete
#cross-references MUID:78114026
#molecule_type protein
#organism Mus musculus #common_name house mouse
#date 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change
17-Mar-1993
#cross-references A44786
#authors Koppe, R.I.; Hallauer, P.L.; Karpati, G.; Hastings, K.E.M.
#journal J. Biol. Chem. (1989) 264:14327-14333
#title cDNA clone and expression analysis of rodent fast and slow
skeletal muscle troponin I mRNAs.

#cross-references MUID:89440548
#accession A44786
#status preliminary
##molecule_type mRNA
##residues 1-182 ##label KOP
#cross-references GB:04992; NID:9202164; PID:9202165
#classification #superfamily troponin I
#keywords skeletal muscle
#summary #length 182 #molecular_weight 21357 #checksum 306

Query Match 30.1% Score 205; DB 2; Length 182;
Best Local Similarity 41.3%; Pred. No. 3.49e-17;
Matches 26; Conservative 20; Mismatches 16; Indels 1; Gaps 1;
#cross-references MUID:78114026
#molecule_type protein
#organism Mus musculus #common_name house mouse
#date 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change
17-Mar-1993
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#cross-references MUID:78114026
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Matches 26; Conservative 20; Mismatches 16; Indels 1; Gaps 1;
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#organism Mus musculus #common_name house mouse
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#cross-references MUID:78114026
#molecule_type protein
#organism Mus musculus #common_name house mouse
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#classification #superfamily troponin I
#keywords skeletal muscle
#summary #length 182 #molecular_weight 21357 #checksum 306

```



OC EUKARYOTA; METAZOA; CHORDATA; UROCHORDATA; ASCIDIACEA; STOLIDOBANCHIA; OC PYURIDAE; HALOCYNTHIA. RN SEQUENCE FROM N.A. RN MEDLINE; 98021076. RX YUSA H.J.; SATO S.; YAMAMOTO H.; TAKAGI T.; RT "Primary structure of troponin I isoforms from the ascidian Halocynthia roretzii." RT J. BIOCHEM. 122:374-380(1997). DR EMBL; AB001686; D1020179; -. DR PFAM; PF00992; Troponin; 1. SQ SEQUENCE 142 AA; 16883 MW; 937073BB CRC32;	Query Match 28.3%; Score 193; DB 5; Length 173; Best Local Similarity 44.6%; Pred. No. 1.43e-16; Matches 25; Conservative 16; Mismatches 14; Indels 1; Gaps 1; RN
Db 5 RKKNLKSLMLNKAREDLKREAEVKAEEKKKILNSRTEPLSNLGGMSQDQLKDLCRE 60 QY 45 RKLQLKTLQIQLQAKQELEREERRGEKGRLSTRCOP-ELAGLGFAELQDLCRQ 99	Db 5 RKKNLKSLMLNKAREDLKREAEVKAEEKKKILNSRTEPLSNLGGMSQDQLKDLCRE 60 QY 45 RKLQLKTLQIQLQAKQELEREERRGEKGRLSTRCOP-ELAGLGFAELQDLCRQ 99
RESULT 5 PRELIMINARY; PRT; 229 AA. ID 077010 PRELIMINARY; PRT; 229 AA. AC 077010; 077010; 08, CREATED) DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE) DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)	RESULT 5 PRELIMINARY; PRT; 229 AA. ID 077010 PRELIMINARY; PRT; 229 AA. AC 077010; 077010; 08, CREATED) DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE) DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
Query Match 30.8%; Score 210; DB 5; Length 142; Best Local Similarity 46.4%; Pred. No. 1.54e-19; Matches 26; Conservative 17; Mismatches 12; Indels 1; Gaps 1; RN	Query Match 30.8%; Score 210; DB 5; Length 142; Best Local Similarity 46.4%; Pred. No. 1.54e-19; Matches 26; Conservative 17; Mismatches 12; Indels 1; Gaps 1; RN
Db 5 RKLQLKSLMLNKAREDLKREAEVKAEEKKKILNSRTEPLSNLGGMSQDQLKDLCRE 60 QY 45 RKLQLKTLQIQLQAKQELEREERRGEKGRLSTRCOP-ELAGLGFAELQDLCRQ 99	Db 5 RKLQLKSLMLNKAREDLKREAEVKAEEKKKILNSRTEPLSNLGGMSQDQLKDLCRE 60 QY 45 RKLQLKTLQIQLQAKQELEREERRGEKGRLSTRCOP-ELAGLGFAELQDLCRQ 99
RESULT 3 PRELIMINARY; PRT; 142 AA. ID 001356 PRELIMINARY; PRT; 142 AA. AC 001356; 001356; 04, CREATED) DT 01-JUL-1997 (TREMBLREL. 04, CREATED) DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)	RESULT 3 PRELIMINARY; PRT; 142 AA. ID 001356 PRELIMINARY; PRT; 142 AA. AC 001356; 001356; 04, CREATED) DT 01-JUL-1997 (TREMBLREL. 04, CREATED) DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
Query Match 30.6%; Score 209; DB 5; Length 142; Best Local Similarity 48.2%; Pred. No. 2.31e-19; Matches 27; Conservative 15; Mismatches 13; Indels 1; Gaps 1; RN	Query Match 30.6%; Score 209; DB 5; Length 142; Best Local Similarity 48.2%; Pred. No. 2.31e-19; Matches 27; Conservative 15; Mismatches 13; Indels 1; Gaps 1; RN
Db 5 RKLQLKSLMLNKAREDLKREAEVKAEEKKKILNSRTEPLSNLGGMSQDQLKDLCRE 60 QY 45 RKLQLKTLQIQLQAKQELEREERRGEKGRLSTRCOP-ELAGLGFAELQDLCRQ 99	Db 5 RKLQLKSLMLNKAREDLKREAEVKAEEKKKILNSRTEPLSNLGGMSQDQLKDLCRE 60 QY 45 RKLQLKTLQIQLQAKQELEREERRGEKGRLSTRCOP-ELAGLGFAELQDLCRQ 99
RESULT 4 PRELIMINARY; PRT; 173 AA. ID 001354 PRELIMINARY; PRT; 173 AA. AC 001354; 001354; 04, CREATED) DT 01-JUL-1997 (TREMBLREL. 04, CREATED) DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)	RESULT 4 PRELIMINARY; PRT; 173 AA. ID 001354 PRELIMINARY; PRT; 173 AA. AC 001354; 001354; 04, CREATED) DT 01-JUL-1997 (TREMBLREL. 04, CREATED) DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
Query Match 23.9%; Score 163; DB 13; Length 176; Best Local Similarity 36.7%; Pred. No. 1.73e-11; Matches 22; Conservative 19; Mismatches 18; Indels 1; Gaps 1; RN	Query Match 23.9%; Score 163; DB 13; Length 176; Best Local Similarity 36.7%; Pred. No. 1.73e-11; Matches 22; Conservative 19; Mismatches 18; Indels 1; Gaps 1;
Db 5 KMTTHORKMMKSLMLNKAREDLKREMEQKAEARKAELSORLPLSGLNSMSSQELMDLCR 115 QY 40 KISASRKQLKTLQIQLQAKQELEREERRGEKGRLSTRCOP-ELAGLGFAELQDLCR 98	Db 5 KMTTHORKMMKSLMLNKAREDLKREMEQKAEARKAELSORLPLSGLNSMSSQELMDLCR 115 QY 40 KISASRKQLKTLQIQLQAKQELEREERRGEKGRLSTRCOP-ELAGLGFAELQDLCR 98
Query Match 26.4%; Score 180; DB 5; Length 229; Best Local Similarity 41.8%; Pred. No. 2.43e-14; Matches 25; Conservative 15; Mismatches 20; Indels 1; Gaps 1; RN	Query Match 26.4%; Score 180; DB 5; Length 229; Best Local Similarity 41.8%; Pred. No. 2.43e-14; Matches 25; Conservative 15; Mismatches 20; Indels 1; Gaps 1; RN
Db 56 KMTTHORKMMKSLMLNKAREDLKREMEQKAEARKAELSORLPLSGLNSMSSQELMDLCR 115 QY 40 KISASRKQLKTLQIQLQAKQELEREERRGEKGRLSTRCOP-ELAGLGFAELQDLCR 98	Db 56 KMTTHORKMMKSLMLNKAREDLKREMEQKAEARKAELSORLPLSGLNSMSSQELMDLCR 115 QY 40 KISASRKQLKTLQIQLQAKQELEREERRGEKGRLSTRCOP-ELAGLGFAELQDLCR 98
Query Match 26.4%; Score 180; DB 5; Length 229; Best Local Similarity 41.8%; Pred. No. 2.43e-14; Matches 25; Conservative 15; Mismatches 20; Indels 1; Gaps 1; RN	Query Match 26.4%; Score 180; DB 5; Length 229; Best Local Similarity 41.8%; Pred. No. 2.43e-14; Matches 25; Conservative 15; Mismatches 20; Indels 1; Gaps 1; RN
Db 116 E 116 QY 99 Q 99	Db 116 E 116 QY 99 Q 99
RESULT 6 PRELIMINARY; PRT; 176 AA. ID 090365 PRELIMINARY; PRT; 176 AA. AC 090365; 090365; 01, CREATED) DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)	RESULT 6 PRELIMINARY; PRT; 176 AA. ID 090365 PRELIMINARY; PRT; 176 AA. AC 090365; 090365; 01, CREATED) DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
Query Match 23.9%; Score 163; DB 13; Length 176; Best Local Similarity 36.7%; Pred. No. 1.73e-11; Matches 22; Conservative 19; Mismatches 18; Indels 1; Gaps 1; RN	Query Match 23.9%; Score 163; DB 13; Length 176; Best Local Similarity 36.7%; Pred. No. 1.73e-11; Matches 22; Conservative 19; Mismatches 18; Indels 1; Gaps 1;
Db 5 KMTSSRKHKHUSKSYMLIAATRLEQAADATAAKETYLPSNDPSTSIEDLQKLCKE 63 QY 40 KISASRKQLKTLQIQLQAKQELEREERRGEKGRLSTRCOP-ELAGLGFAELQDLCR 99	Db 5 KMTSSRKHKHUSKSYMLIAATRLEQAADATAAKETYLPSNDPSTSIEDLQKLCKE 63 QY 40 KISASRKQLKTLQIQLQAKQELEREERRGEKGRLSTRCOP-ELAGLGFAELQDLCR 99
RESULT 7	RESULT 7

AC	013095;	PRELIMINARY;	PRT;	172 AA.	RC	STRAIN=CLYDE-STOCK (BUCHAN BANK); TISSUE=WHOLE ORGANISM;
DT	01-JUL-1997	(TREMBLREL. 04, CREATED)	RA	HODGSON P.A., LEAVER M.J., GEORGE S.G., MACLEAN D.W.,		
DT	01-JUL-1997	(TREMBLREL. 04, LAST SEQUENCE UPDATE)	RA	HASTINGS K.E.M.;		
DT	01-NOV-1998	(TREMBLREL. 08, LAST ANNOTATION UPDATE)	RL	SUBMITTED (JAN-1995) TO EMBL/GENBANK/DBBJ DATA BANKS.		
DE	TROPONIN-I	ISOFORM 3.	DR	EMBL; U20112; GI1020148;		
OS	SALMO SALAR (ATLANTIC SALMON).	DR	PFAM; PF00992; Troponin 1.			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII; TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; SALMONIFORMES; SALMONIDAE; SALMO.	SQ	SEQUENCE 176 AA; 19805 MW; F452B8B3 CRC32;			
RN	[1]				Query Match	22.3%; Score 152; DB 13; Length 176;
RP	SEQUENCE FROM N.A.				Best Local Similarity	41.7%; Pred No. 1.10e-09;
RC	TISSUE=MYOTOMAL MUSCLE;				Matches	25; Conservative 13; Mismatches 21; Indels 1; Gaps 1;
RA	WADDLETON D.M., JACKMAN D.M./BIEGER T., NOEL J.J., HEELEY D.H.;					
RL	SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBBJ DATA BANKS.					
DR	EMBL; U84394; G2062499; -					
PFAM;	PF00992; Troponin 1.					
DR	PFAM; PF00992; Troponin 1.					
SEQ	SEQUENCE 172 AA; 19390 MW; F5187036 CRC32;					
RESULT	10	PRELIMINARY;	PRT;	172 AA.	RESULT	10
ID	013093	PRELIMINARY;	PRT;	172 AA.	ID	013093
AC	013093;				AC	013093;
DT	01-JUL-1997	(TREMBLREL. 04, CREATED)	RC	TISSUE=IMMATURE WHOLE MYOTOMAL MUSCLE;		
DT	01-JUL-1997	(TREMBLREL. 04, LAST SEQUENCE UPDATE)	RA	WADDLETON D.M., BIEGER T., NOEL J.J., HEELEY D.H.;		
DT	01-NOV-1998	(TREMBLREL. 08, LAST ANNOTATION UPDATE)	RL	SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBBJ DATA BANKS.		
DB	5 KMTSSRKHLKSLMLIAKDLKEAADLITEKAIFIACNPAVLSG-GLPELQEM 60	DR	EMBL; U84397; G2062473; -			
QY	40 KISASRKLQLKTLQIAKQELEREAEERRGKGRALSTRCQPLDELAGLFAELQL 96	DR	PFAM; PF00992; Troponin 1.			
SEQ	SEQUENCE 172 AA; 19390 MW; F5187036 CRC32;	SQ	SEQUENCE 172 AA; 19781 MW; 192ACAFA CRC32;			
RESULT	8	PRELIMINARY;	PRT;	180 AA.	Query Match	17.2%; Score 117; DB 13; Length 172;
ID	013094	PRELIMINARY;	PRT;	180 AA.	Best Local Similarity	37.5%; Pred No. 2.99e-04;
AC	013094;				Matches	18; Conservative 14; Mismatches 15; Indels 1; Gaps 1;
DT	01-JUL-1997	(TREMBLREL. 04, CREATED)	RP	SEQUENCE FROM N.A.		
DT	01-JUL-1997	(TREMBLREL. 04, LAST SEQUENCE UPDATE)	RC	TISSUE=IMMATURE WHOLE MYOTOMAL MUSCLE;		
DT	01-NOV-1998	(TREMBLREL. 08, LAST ANNOTATION UPDATE)	RA	WADDLETON D.M., BIEGER T., NOEL J.J., HEELEY D.H.;		
DB	5 KMTSSRKHLKSLMLIAKDLKEAADLITEKAIFIACNPAVLSG-GLPELQEM 60	RL	SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBBJ DATA BANKS.			
QY	40 KISASRKLQLKTLQIAKQELEREAEERRGKGRALSTRCQPLDELAGLFAELQL 96	DR	EMBL; U84397; G2062473; -			
SEQ	SEQUENCE 180 AA; 20954 MW; BD74CFD3 CRC32;	DR	PFAM; PF00992; Troponin 1.			
RESULT	8	PRELIMINARY;	PRT;	180 AA.	DB	5 RMTSSRKHLKSLMLQIAANLIEREKKENKQEKYNFMANI-PALDLSG 51
ID	013094	PRELIMINARY;	PRT;	180 AA.	QY	40 KISASRKLQLKTLQIAKQELEREAEERRGKGRALSTRCQPLDELAGLFAELQL 87
AC	013094;				SEQ	SEQUENCE 180 AA; 20954 MW; BD74CFD3 CRC32;
DT	01-JUL-1997	(TREMBLREL. 04, CREATED)	RESULT	11		
DT	01-JUL-1997	(TREMBLREL. 04, LAST SEQUENCE UPDATE)	ID	075420		
DT	01-NOV-1998	(TREMBLREL. 08, LAST ANNOTATION UPDATE)	AC	075420;		
DB	2 ADKRNVSSRKHLKSLMLAKDLWEALEKVERYMAENCPLSMS-HSKEDLM 60	RT	"Large scale analysis of two regions in human chromosome 7q22; annotation of 650 kb of genomic sequence around the PCOLCE and CUTL1 loci reveals 17 genes."			
QY	35 AKKSKKISASRKLQLKTLQIAKQELEREAEERRGKGRALSTRCQPLDELAGLFAELQL 94	DT	DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)			
SEQ	SEQUENCE 180 AA; 20954 MW; BD74CFD3 CRC32;	OS	OS HOMO SAPIENS (HUMAN).			
DE	61 ELCK 64	OC	OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.			
QY	95 DCLC 98	RN	RN [1]			
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.			
RC	TISSUE=MYOTOMAL MUSCLE;	RA	GLOECKNER G., ROSENTHAL A., SCHERER S., WEBER J., SCHATTEVOY R., TSUI L.-C.;			
RA	WADDLETON D.M., JACKMAN D.M./BIEGER T., NOEL J.J., HEELEY D.H.;	RT	RT Large scale analysis of two regions in human chromosome 7q22; annotation of 650 kb of genomic sequence around the PCOLCE and CUTL1 loci reveals 17 genes."			
RL	SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBBJ DATA BANKS.	RT	RT Large scale analysis of two regions in human chromosome 7q22; annotation of 650 kb of genomic sequence around the PCOLCE and CUTL1 loci reveals 17 genes."			
DR	EMBL; U84394; G2062497; -	DR	DR SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBBJ DATA BANKS.			
PFAM;	PFAM; PF00992; Troponin 1.	SQ	SQ AF053356; G313508; -			
DR	PFAM; PF00992; Troponin 1.	SEQ	SEQ 817 AA; 89740 MW; 284A8182 CRC32;			
SEQ	SEQUENCE 180 AA; 20954 MW; BD74CFD3 CRC32;	Query Match	15.5%; Score 106; DB 4; Length 817;			
RESULT	9	PRELIMINARY;	PRT;	176 AA.	Best Local Similarity	30.4%; Pred No. 1.14e-02;
ID	090366	PRELIMINARY;	PRT;	176 AA.	Matches	29; Conservative 28; Mismatches 28; Indels 7; Gaps 7;
AC	090366;					
DT	01-NOV-1996	(TREMBLREL. 01, CREATED)				
DT	01-NOV-1996	(TREMBLREL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1998	(TREMBLREL. 08, LAST ANNOTATION UPDATE)				
DE	TROPONIN-I.					
CS	CLUPEA HARENGUS (ATLANTIC HERRING).					
CC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII; CLUPEIDAE.					
CC	CLUPEA; CLUPEOMORPHA; CLUPEIDAE.					
RN	[1]					
RP	SEQUENCE FROM N.A.					

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EMBL; X5163; G37428; ALT\_SEQ.

EMBL; M64247; G339967; \_.

EMBL; X90780; E196058; \_.

EMBL; X90781; E196058; JOINED.

EMBL; X90782; E196058; JOINED.

PIR; A61229; A61229.

PIR; 191044; PIR; 1.

PFAM; PF00992; Troponin; 1.

DR MUSCLE PROTEIN; ACTIN-BINDING; ACETYLATION.

FT INIT-MET 0 ACETYLATION (BY SIMILARITY).

FT MOD-RES 1 INVOLVED IN TNI-TNT INTERACTIONS.

FT STATE 79 INVOLVED IN TNI-TNT INTERACTIONS.

FT SITE 79 INVOLVED IN BINDING TNC.

FT DOMAIN 31 INVOLVED IN BINDING TNC AND ACTIN.

FT DOMAIN 128 INVOLVED IN BINDING TNC.

FT SEQUENCE 209 AA; 23876 MW; 2E5B1B3 CRC32;

Query Match 98.4%; score 671; DB 1; Length 209;

Best Local Similarity 100.0%; Pred. No. 1.6e-116; Gaps 0;

Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ADGSSDAAREPRPAPAPIRRSSNRYAYATEPHAKKSISASKRQLQLQIAKQEL 60

1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

2 ADGSSDAAREPRPAPAPIRRSSNRYAYATEPHAKKSISASKRQLQLQIAKQEL 61

1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 EREAERGERGEKGRALSTRCOPPLELAGLGFAELQDLCRQ 98

1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 62 EREAERGERGEKGRALSTRCOPPLELAGLGFAELQDLCRQ 99

1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2 TRIC\_MOUSE STANDARD; PRT; 210 AA.

ID P8787; PRT; 210 AA.

AC DT 01-FEB-1996 (REL. 33, CREATED)

AC DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)

AC DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE TROPONIN I, CARDIAC MUSCLE.

GN TNNI3.

OS MUS MUSCULUS (MOUSE).

OC EUDORYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC RODENTIA; SCUTROGNATHI; MURIDAE; MORINAE; MUS.

RN [1]

RP SEQUENCE FROM N.A.

RP STRAIN=CD-1; TISSUE=HEART;

RC MEDLINE; 94103233.

RX AUISONI S., CAMPIONE M., PICARD A., MORETTI P., VITTADELLO M., SOLARO R.J.;

RA GUO X., WATANAPERNPOL J., PALMITER K.A., MURPHY A.M., SOLARO R.J.;

RA DE NARDI C., SCHIAFFINO S.;

RT "Muragenesis of cardiac tropomodulin I. Role of the unique NH2-terminal structure and regulation of the mouse cardiac tropomodulin I gene.";

RL J. BIOL. CHEM. 269:3339-3346(1994).  
[2]

RN SEQUENCE FROM N.A.

RC MEDLINE; 94253083.

RX GUO X., WATANAPERNPOL J., PALMITER K.A., MURPHY A.M., SOLARO R.J.;

RA DE NARDI C., SCHIAFFINO S.;

RT "Muragenesis of cardiac tropomodulin I. Role of the unique NH2-terminal structure and regulation of the mouse cardiac tropomodulin I gene.";

RL J. BIOL. CHEM. 269:15210-15164(1994).  
[3]

CC -1- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERs CALCIUM-SENSITIVITY TO STIMULATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.

CC -1- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.

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Db	1	ADGSSDAAREPAPAPIRRSSNRYATEPHAKKSKTSASRKLQLKTLQLQIAKQEL 60
Qy	2	ADGSSDAAREPAPAPIRRSSNRYATEPHAKKSKTSASRKLQLKTLQLQIAKQEL 61
Db	61	ERAEAEERGEKGKGRALSTRCOPLELAGLGFAELQDLICRQ 98
Qy	62	ERAEAEERGEKGKGRALSTRCOPLELAGLGFAELQDLICRQ 99

RESULT	2	STANDARD	PRT;	210 AA.
ID	TRIC_MOUSE			
AC	P48187;			
DT	01-FEB-1996	(REL. 33, CREATED)		
DT	01-FEB-1996	(REL. 33, LAST SEQUENCE UPDATE)		
DT	01-FEB-1996	(REL. 33, LAST ANNOTATION UPDATE)		
DE	TRIOPONIN I,	CARDIAC MUSCLE.		
GN	TNNI3.			
OS	MUS MUSCULUS (MOUSE)			
REVDAT	2002-07-01			
CHORDATA				
VERTEBRATA				
MAMMALIA				
EUTHERIA				

OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.  
 RN [1]  
 RX SEQUENCE FROM N. A.  
 RX MEDLINE; 94103233.  
 RA AUSONI S., PICARD M., MORETTI P., VITTADELLO M.,  
 RA DE NARDI C., SCHIAFFINO S.;  
 RT "Structure and regulation of the mouse cardiac troponin I gene,"  
 RT *Journal of Molecular Biology* 252:220-245 (1994).

[2] RN SEQUENCE FROM N.A.  
RP SEQUENCE-CD-1; TISSUE-HEART;  
RC STRAIN-CD-1;  
RX MEDINE; 94251083.  
RA GUO X.; WATTANAPERAPPOOL J.; PALMITER R.A.; MURPHY A.M.; SOLARO R.J.;  
RT "Mutagenesis of cardiac troponin I. Role of the unique NH2-terminal

PF500 -  
RL J. BIOL. CHEM. 269:15210-15216(1994).  
CC -I: FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE  
CC THIN FILAMENT REGULATORY COMPLEX WHICH CONFERs CALCIUM-SENSITIVITY  
CC TO SRRATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.  
CC -I: TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.  
CC

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FT	NON_TER	168 AA;	18979 MW;	F25BBADF CRC32;				
Query Match	39.3%	Score 268;	DB 1;	Length 188;				
Best Local Similarity	68.5%	Pred. No. 4.71e-32;						
Matches	37;	Conservative	6;	Mismatches 11;	Indels 0;	Gaps 0;		
Db	1	KLQLKTLIQLQAKRPLEREFQERAGEKQRHGGCQPPELEGLGVAQLOBLCRE 54						
Qy	46	KLQLKTLIQLQAKQELEREAEERRGEKGRALSTRQPLELAGLGFAEQLDLCRQ 99						
RESULT	9							
ID	TRIS_RAT	STANDARD;	PRT;	186 AA.				
AC	P13413;							
DT	01-JAN-1990 (REL. 13, CREATED)							
DT	01-FEB-1996 (REL. 13, LAST ANNOTATION UPDATE)							
DE	TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM)							
DE	TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM)							
OS	RATTUS NORVEGICUS (RAT)							
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUThERIA;							
OC	RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RC	TISSUE=BLOOD;							
RX	MEDLINE: 94193765.							
RA	CORBIN S.J., JUHASZ O., CONLEY P., ZHU L., KEDES L., KEDES R., WADE R.;							
RT	"Structure and expression of the human slow twitch skeletal muscle troponin I gene."							
RT	J. BIOL. CHEM. 269:10651-10659(1994).							
CC	-!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERs CALCIUM-SENSITIVITY							
CC	TO SPINATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.							
CC	-!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.							
CC	RP SEQUENCE FROM N.A.							
RX	MEDLINE: 89340548.							
RA	KOPPE R.I., HALLAUER P.L., KARPATI G., HASTINGS K.E.M.;							
RT	"cDNA clone and expression analysis of rodent fast and slow skeletal muscle troponin I mRNAs."							
RT	J. BIOL. CHEM. 264:14327-14331(1989).							
CC	-!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERs CALCIUM-SENSITIVITY							
CC	TO SPINATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.							
CC	-!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.							
CC	RP SEQUENCE FROM N.A.							
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - "cDNA Clone and expression analysis of rodent fast and slow skeletal muscle troponin I mRNAs".							
CC	J. BIOL. CHEM. 264:14327-14331(1989).							
CC	-!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERs CALCIUM-SENSITIVITY							
CC	TO SPINATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.							
CC	-!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.							
CC	RP SEQUENCE FROM N.A.							
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - "cDNA Clone and expression analysis of rodent fast and slow skeletal muscle troponin I mRNAs".							
CC	J. BIOL. CHEM. 264:14327-14331(1989).							
CC	-!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERs CALCIUM-SENSITIVITY							
CC	TO SPINATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.							
CC	-!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.							
DR	B44786; G207518; -.							
DR	PFAM; PF00992; Tropomin; 1.							
KW	MUSCLE PROTEIN; ACTIN-BINDING.							
FT	INIT MET 0	0						
FT	DOMAIN 1	47						
FT	DOMAIN 96	117						
SQ	SEQUENCE 186 AA; 21593 MW; C12529CD CRC32;							
Query Match	34.8%	Score 237;	DB 1;	Length 186;				
Best Local Similarity	53.7%	Pred. No. 5.03e-26;						
Matches	36;	Conservative 12;	Mismatches 19;	Indels 0;	Gaps 0;			
Db	1 PEVERKSKITASRKIIMLKSLMLAKAKECQEHEERAEAKVYRLSERIPTLQTCRGLSLSA 60							
Qy	33 PHAKKKSKTISASRKIQLKTLQIAKQELEREAEERRGEKGRALSTRCOPPLELAGLGFAE 92							
Db	61 LDLGCRE 67							
Qy	93 LDLGCRE 99							
RESULT	11							
ID	TRIS_RABBIT	STANDARD;	PRT;	184 AA.				
AC	P02645;							
DT	21-JUL-1986 (REL. 01, CREATED)							
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)							
DT	01-FEB-1986 (REL. 33, LAST ANNOTATION UPDATE)							
DE	TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM).							
GN	TNNIL.							
OS	ORYCTOLAGUS CUNICULUS (RABBIT),							
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUThERIA;							
OC	LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.							
RN	[1]							
RP	SEQUENCE.							
RX	MEDLINE: 78060292.							



RL	SUBMITTED (XXX-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC	-!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFFERS CALCIUM-SENSITIVITY
CC	-!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
CC	-----
RESULT 13	STANDARD; PRT; 181 AA.
ID TRIF_MOUSE	STANDARD; PRT; 181 AA.
AC P13412;	SEQUENCE FROM N.A.
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)	MDLINE; P834054R.
DT 01-JAN-1990 (REL. 13, LAST ANNOTATION UPDATE)	RA KOPPE R.I., HALLAER P.L., KARPATI G., HASTINGS K.E.M.;
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)	RT cDNA clone and expression analysis of rodent fast and slow skeletal muscle tropomyosin mRNAs.";
DE TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM).	J. BIOL. CHEM. 26:11327-14323 (1989).
GN TNNI2.	-!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFFERS CALCIUM-SENSITIVITY
OS MUS MUSCULUS (MOUSE).	CC TO SRRATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	-!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
RODENTIA; SCIUROGNATHI; MURIDAE; MURINA; MUS.	CC
[1]	RN SEQUENCE FROM N.A.
RP	DR EMBL: M73701; G206885; -.
RX	DR PFAM: PF00992; Tropomin; 1.
RA HSSP: P02643; 1A2X.	DR HSSP: P02643; 1A2X.
RT	MUSCLE PROTEIN; ACTIN-BINDING.
FT INIT-MET	KW 0 BY SIMILARITY.
FT DOMAIN	FT 47 INVOLVED IN BINDING TNC.
FT DOMAIN	FT 96 INVOLVED IN BINDING TNC AND ACTIN.
SQ SEQUENCE	FT 181 AA; D0DDEFA8 CRC32;
-----	-----
Query Match	Score 203; DB 1; Length 181;
Best Local Similarity	Score 203; DB 1; Length 181;
Matches 26; Conservative 20; Mismatches 16; Indels 1; Gaps 1;	Pred. No. 1.37e-19.
-----	-----
Db 5 KRNRAITARRQHLKSYMLOQIAATELEKEERSEKEVYSEHCPPLHIG-SMSEVOEL 63	RESULT 15
Qy 37 KKS KISASRKQLQLKTLIQAKQELEREAEERGKRALSTRCOPLEAGLGFLQLD 96	ID TRIF_HUMAN STANDARD; PRT; 181 AA.
-----	ID P48788;
Db 5 KRNRAITARRQHLKSYMLOQIAATELEKEERSEKEVYSEHCPPLHIG-SMSEVOEL 63	AC PF00992 (REL. 33, CREATED)
Qy 37 KKS KISASRKQLQLKTLIQAKQELEREAEERGKRALSTRCOPLEAGLGFLQLD 96	DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
-----	DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
Db 64 CKQ 66	DE TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM).
Qy 97 CRQ 99	GN TNNI2.
-----	OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.	CC SEQUENCE FROM N.A.
DR PIR: J04982; G202165; -.	DR TISSUE-SKELETAL, MUSCLE;
DR MGI: MGI:105070; TNNI2.	DR MEDLINE; 9A198300.
DR PFAM: PF00992; Tropomin; 1.	RA ZHU L., PEREZ-ALVARADO G., WADE R.;
DR HSSP: P02643; 1A2X.	RA "Sequencing of a cDNA encoding the human fast-twitch skeletal muscle isoform of tropomin I,"
KW MUSCLE PROTEIN; ACTIN-BINDING.	RT BIOCML. BIOPHYS. ACTA 1217:338-340 (1994).
FT INIT-MET	RL
FT DOMAIN	CC -!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFFERS CALCIUM-SENSITIVITY
FT DOMAIN	CC TO SRRATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
SQ SEQUENCE	CC -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
-----	CC
Query Match	Score 205; DB 1; Length 181;
Best Local Similarity	Score 205; DB 1; Length 181;
Matches 26; Conservative 20; Mismatches 16; Indels 1; Gaps 1;	Pred. No. 5.81e-20.
-----	RN SEQUENCE FROM N.A.
Db 5 KRNRAITARRQHLKSYMLOQIAATELEKEERSEKEVYSEHCPPLHIG-SMSEVOEL 63	DR TISSUE-SKELETAL, MUSCLE;
Qy 37 KKS KISASRKQLQLKTLIQAKQELEREAEERGKRALSTRCOPLEAGLGFLQLD 96	DR MEDLINE; 9A198300.
-----	RA ZHU L., PEREZ-ALVARADO G., WADE R.;
Db 64 CKQ 66	RA "Sequencing of a cDNA encoding the human fast-twitch skeletal muscle isoform of tropomin I,"
Qy 97 CRQ 99	RT BIOCML. BIOPHYS. ACTA 1217:338-340 (1994).
-----	RL
RESULT 14	CC -!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFFERS CALCIUM-SENSITIVITY
ID TRIF_RAT	CC TO SRRATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
AC P27768;	CC -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
DT 01-AUG-1992 (REL. 23, CREATED)	CC
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)	CC
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)	CC
DE TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM).	CC
DE TNNI2 OR TRP1.	CC
GN RATTUS NORVEGICUS (RAT).	CC
OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;	CC
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINA; RATTUS.	CC
[1]	RN SEQUENCE FROM N.A.
RP	DR EMBL: L21715; G452078; -.
RA	DR PFAM: PF00992; Tropomin; 1.
RA HSSP: P02643; 1A2X.	DR KW MUSCLE PROTEIN; ACTIN-BINDING.

FT	INIT-MET	0	0	BY SIMILARITY.
FT	DOMAIN	1	47	INVOLVED IN BINDING TNC.
FT	DOMAIN	96	116	INVOLVED IN BINDING TNC AND ACTIN.
FT	SEQUENCE	181 AA:	21207 MW:	83ED65E4 CRC32:
SQ				
Query Match		29.5%	Score 201;	DB 1; Length 181;
Best Local Similarity	39.7%	Pred. No. 3.22e-19;		
Matches	25;	Conservative 21;	Mismatches 16;	Indels 1; Gaps 1;
Db	5	KRNRAITARRQHLKSVMLQIAATELEKEESRREAENQYLAEHCPPLHFG-SMSEVQEL	63	
Qy	37	KRSKISASRKQLQLKTLQIAKQELEREAEERRGEKGRAALSTRCOPFLAGLGFELQDL	96	
Db	64	CKQ	66	
Qy	97	CRQ	99	